\_\_\_\_\_

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=1; day=8; hr=10; min=22; sec=40; ms=875; ]

\_\_\_\_\_\_

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

Reviewer Comments:

Glu Leu Leu Asn Ser Met Asn. Ile Ser Gln Pro Thr Val Val Phe Val
115 120 125

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val 370 380

Please delete invalid alpha numeric character appearing beside amino acid coding Asn at position 119 in the above sequence id# 39. Please also correct invalid amino acid numbering appearing above at positiom 375 in the sequence, please check the remaining sequences for similar errors.

Phe Lue Arg Ser Lue Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val 275 280 285

Please also correct invalid amino acid coding Lue appearing at position 274 and 277 in the above sample of sequence id# 41.

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
65 70 75 80

Pro Ile Phe Gly ASn Gln Ile Xaa Pro Asp Thr Ala Ile Leu Ser Val 225 230 235 240 Per the above sample of sequence id# 42, please correct invalid amino acid numbering at position 75 in the sequence. Please also correct invalid amino acid coding ASn at position 229 in the sequence.

\*\*\*\*\*\*\*\*\*\*\*\*\*

## Validated By CRFValidator v 1.0.3

Application No: 09763824 Version No: 5.0

Input Set:

## Output Set:

**Started**: 2008-12-24 10:25:15.658

Finished: 2008-12-24 10:25:19.413

**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 755 ms

Total Warnings: 36

Total Errors: 8

No. of SeqIDs Defined: 42

Actual SeqID Count: 42

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W	213	Artificial or	Unknown	found	in	<213>	in	SEQ	ID	(12)
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W	213	Artificial or	Unknown	found	in	<213>	in	SEQ	ID	(18)
W	213	Artificial or	Unknown	found	in	<213>	in	SEQ	ID	(19)
W	213	Artificial or	Unknown	found	in	<213>	in	SEQ	ID	(20)

## Input Set:

## Output Set:

**Started:** 2008-12-24 10:25:15.658 **Finished:** 2008-12-24 10:25:19.413

**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 755 ms

Total Warnings: 36
Total Errors: 8
No. of SeqIDs Defined: 42

Actual SeqID Count: 42

Error code		Error Description								
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E	330	Invalid protein , found in SEQID(39) POS (119) Invalid								
E	323	Invalid/missing amino acid numbering SEQID (39)at Protein (375)								
E	323	Invalid/missing amino acid numbering SEQID (39) POS (376)								
E	330	Invalid protein , found in SEQID(41) POS (274) Invalid Protein: Lue								
E	330	Invalid protein , found in SEQID(41) POS (277) Invalid Protein: Lue								
E	323	Invalid/missing amino acid numbering SEQID (42) POS (73)								
E	323	Invalid/missing amino acid numbering SEQID (42)at Protein (75)								
E	330	Invalid protein , found in SEQID(42) POS (229) Invalid Protein: ASn								

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MURPHY, MELANIE J.
PRICE, RACHEL L.
LOWE, CHRISTOPHER R.
WHITE, PETER J.
TISI, LAURENCE C.
MURRAY, JAMES A. H .
<120> NOVEL ENZYME
<130> 1498-119
<140> 09763824
<141> 2001-02-27
<150> PCT/GB99/03538
<151> 1999-10-26
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<110> SQUIRRELL, DAVID J.

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     50
                         55
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Phe	Ile	Gly	Val 100	Ala	Val	Ala	Pro	Ala 105	Asn	Asp	Ile	Tyr	Asn 110	Glu	Arg
Glu	Leu	Leu 115	Asn	Ser	Met	Asn	Ile 120	Ser	Gln	Pro	Thr	Val 125	Val	Phe	Val
Ser	Lys 130	Lys	Gly	Leu	Gln	Lys 135	Ile	Leu	Asn	Val	Gln 140	Lys	Lys	Leu	Pro
Ile 145	Ile	Gln	Lys	Ile	Ile 150	Ile	Met	Asp	Ser	Lys 155	Thr	Asp	Tyr	Gln	Gly 160
Phe	Gln	Ser	Met	Tyr 165	Thr	Phe	Val	Thr	Ser 170	His	Leu	Pro	Pro	Gly 175	Phe
Asn	Glu	Tyr	Asp 180	Phe	Val	Pro	Glu	Ser 185	Phe	Asp	Arg	Asp	Lys 190	Thr	Ile
Ala	Leu	Ile 195	Met	Asn	Ser	Ser	Gly 200	Ser	Thr	Gly	Leu	Pro 205	Lys	Gly	Val
Ala	Leu 210	Pro	His	Arg	Thr	Ala 215	Cys	Val	Arg	Phe	Ser 220	His	Ala	Arg	Asp
Pro 225	Ile	Phe	Gly	Asn	Gln 230	Ile	Ile	Pro	Asp	Thr 235	Ala	Ile	Leu	Ser 2	Val 240
Val	Pro	Phe	His	His 245	Gly	Phe	Gly	Met	Phe 250	Thr	Thr	Leu	Gly	Tyr 255	Leu
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Asp 305	Leu	Ser	Asn	Leu	His 310	Glu	Ile	Ala	Ser	Gly 315	Gly	Ala	Pro	Leu	Ser 320
Lys	Glu	Val	Gly	Glu 325	Ala	Val	Ala	Lys	Arg 330	Phe	His	Leu	Pro	Gly 335	Ile
Arg	Gln	Gly	Tyr 340	Gly	Leu	Thr	Glu	Thr 345	Thr	Ser	Ala	Ile	Leu 350	Ile	Thr
Pro	Glu	Gly 355	Asp	Asp	Lys	Pro	Gly 360	Ala	Val	Gly	Lys	Val 365	Val	Pro	Phe

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Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Me 385 390 395	t Ser Gly 400
Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Ly 405 410	s Asp Gly 415
Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Gl 420 425 43	
Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gl 435 440 445	y Tyr Gln
Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro 450 455 460	o Asn Ile
Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly 465 470 475	y Glu Leu 480
Pro Ala Ala Val Val Leu Glu His Gly Lys Thr Met Th 485 490	r Glu Lys 495
Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Ly 500 505 51	_
Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Let 515 520 525	u Thr Gly
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Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg Glu Leu Leu Asn Ser Met Asn Ile Ser Gln Pro Thr Val Val Phe Val Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val Ala Leu Pro His Arg Xaa Ala Cys Val Arg Phe Ser His Ala Arg Asp Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr

Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe

355 360 365

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val 370 375 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly 385 390 395 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly
405 410 415

Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe
420 425 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln
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Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile 450 455 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu 465 470 475 488

Pro Ala Ala Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys
485 490 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu
500 505 510

Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly 515 520 525

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Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu 35 40 45

- Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala 50 55 60
- Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val 65 70 75 80
- Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu 85 90 95
- Phe Ile Gly Val Ala Val Ala Pro Ala As<br/>n Asp Ile Tyr As<br/>n Glu Arg 100 105 110
- Glu Leu Leu Asn Ser Met Asn. Ile Ser Gln Pro Thr Val Val Phe Val 115 120 125
- Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro 130 135 140
- Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly  $\mathbf{1}$